

GTCATATGCTGTTCAGTTCATGCCAATGGCAGCAGCCTCCGGCTCTCTGTCTGGAGTCTCTGGCATCCCGATGGACAACCGGCAGCCAC	90
M L F K S W Q L A A A S G L L S G V L G I P M D T G S H	28
CCCATTGAGGCTGTTCATCCCGAAGTGAAGACTGAGGCTCTTCGCTGACTCCCTCTCTGCTGCAGCAGGCGATGACGACTGGGAGTCACT	180
P I E A V D P E V K T E V F A D S L L A A A G D D D W E S P	58
CCATACAACCTTGCTTTACAGGAATGCCCTGCCAATTCCACTGTCAAGCAGGCCAAGATGATCATTACCAACCTGTCAACGGCAAGGAC	270
P Y N L L Y R N A L P I P P V K Q P K M I I T N P V T G K D	88
ATTTGGTACTATGAGATCGAGATCAAGCCATTTCAGCAAGGATTTACCCCACTTGGCCCTGCCACTCTCTGCTGGCTACGATGCCATG	360
I W Y Y E I E I K P F Q Q R I Y P T L R P A T L V G Y D G M	118
AGCCCTGGTCTACTTTCAATGTTCCCGAGGAAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTGGTCCATCTG	450
S P G P T F N V P R G T E T V V R F I N N A T V E N S V H L	148
CAAGGCTCCCATCGCGTGGCCCTTTGATGGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCCAACTAC	540
H G S P S R A P F D G W A E D V T F P G E Y K D Y Y F P N Y	178
CAATCCGCCCCCTTCTGTGGTACCATGACCACGCTTTTCATGAAGACTGCTGAGAATGCTACTTTGGTTCAGGCTGGCGCTACATTATC	630
Q S A R L L W Y H D H A F M K T A E N A Y F G Q A G A Y I I	208
AACGACGAGGCTGAGGATGCTCTCGGCTCTCTAGTGGCTATGGCGAGTTCGATATCCCTCTGATCTCTGACGCCAAGTACTATAAGCC	720
N D E A E D A L G L P S G Y G E F D I P L I L T A K Y Y N A	238
GATGGTACCCCTGGCTTCGACCGAGGGTGAGGACCAGGACCTGTGGGGAGATGTCATCCATGTCAACGGACAGCCATGGCCCTTTCTTTAAC	810
D G T L R S T E G E D Q D L W G D V I H V N G Q P W P F L N	268
GTCCAGCCCCGCAAGTACCGTTTCGATTTCCTCAACGCTGCCGCTGCTCTGCTGCTTGGCTCTCTACCTCTGTCAGGACCAGCTCTCCCAAC	900
V Q P R K Y R F R F L N A A V S R A W L L Y L V R T S S P N	298
GTCAGAATTCTTTTCCAAGTCATTGCTCTGATGCTGGTCTCTCTTCAAGCCCCGTTTCAGACCTCTAACCTCTACCTTGCTGTTCGCGAG	990
V R I P F Q V I A S D A G L L Q A P V Q T S N L Y L A V A E	328
CGTTACGAGATCATTATTGACTTTCACCAACTTTGCTGGCCAGACTCTTTCACCTTGGCAACGTTGCTGAGACCAACGATGTGGCGACGAG	1080
R Y E I I I D F T N F A G Q T L D L R N V A E T N D V G D E	358
GATGAGTACGCTCGCACCTCTCGAGGTGATGCGCTTCGCTGCTCAGCTCTGGCACTGTTGAGGACAACAGCCAGGTCCCTCCACTCTCGGT	1170
D E Y A R T L E V M R F V V S S G T V E D N S Q V P S T L R	388
GAAGTCTCTTTCCCTCTCTCACAAGGAAGCCCCCGCCGACAAGCACTTCAAGTTTGAACCGAGCAACGGCACTACCTGATCAACGATGTT	1260
D V P F P P H K E G P A D K H F K F E R S N G H Y L I N D V	418
GGCTTTGGCGATGTCAATGAGCGTGTCTGGCCAAAGCCCGAGCTGGCCACCGTTGAGGCTCTGGGAGCTCGAGAACTCTCTGGAGGCTGG	1350
G F A D V N E R V L A K P E L G T V E V W E L E N S S G G W	448
AGCCACCCCGTCCACATTTCACCTTGTTCAGTTCAAGATCTCAAGCGAACTGGTGGTCTGGCCAGGTCATGCCCTACGAGTCTGCTGGT	1440
S H P V H I H L V D F K I L K R T G G R G Q V M P Y E S A G	478
CTTAAGGATGTGCTCTGGTTGGGCAAGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGT	1530
L K D V V W L G R G E T L T I E A H Y Q P W T G A Y M W H C	508
CACAACCTCATTCACGAGGATAACGACATGATGGCTGTATTCAACGTCACCGCCATGGAGGAGAAGGGATATCTTCAGGAGGACTTCGAG	1620
H N L I H E D N D M M A V F N V T A M E E K G Y L Q E D F E	538
GACCCCATGAACCCCAAGTGGCGCGCGCTTCTTACAACCGCAACGACTTCCATGCTCGCGCTGGAACTTCTCCGCGGAGTCCATCACT	1710
D P M N P K W R A V P Y N R N D F H A R A G N F S A E S I T	568
GCCCGAGTGCAGGAGCTGGCCGAGCAGGAGCCGTACAAACCGCTCGATGAGATCTGGAGGATCTTGGAAATCGAGGAGTAA	1791
A R V Q E L A E Q E P Y N R L D E I L E D L G I E E	594

Figure 1


```

1 .....MFKHITLGAALSLFNNAVQA.SVPETSPATGHLFKRV 39
      |         |         |         |         |
1 MLFKSWQLAAASGLLSGVLGITPMDTGSHPIEAVDPEVKTEVFADSLAAA 50

40 AQISPOQYPMFTV....PLPIPPVKQPRLTVINPVGQETIWWYEVEIKPFT 85
      |         |||||         |||         |||||         |||||
51 GDDWESPPYNLLYRNALPIPPVKQPKMITINPVTGKDIWWYEIEIKPFQ 100

86 HQVYPDLGSADLVGYDGMSPGPIFQVPRGVETVWRFINNAEAPNSVHLHG 135
      || | | |||||         |||         |||||         |||||
101 QRIYPTLRPATLVGYDGMSPGPIFNVRGTETVWRFINNATVENSVHLHG 150

136 SFSRAAFDGAEDITEFGSFKDYYPNRQSARTLWYHDHAMHTTAENAYR 185
      | ||| ||||| | || | ||| | ||| |||||         |||||
151 SPSRAPFDGAEDVITFFGEYKDYYPNYQSARLLWYHDHAFMKTAEAYF 200

186 GQAGLYMLTDPADALNLP SGYGEFDIPMLITSKYTANGNLVTINGELN 235
      |||| | | |||||         |||||         |||         |||
201 GQAGAYTINDEAEDALGLPSGYGEFDIPLILITAKYVADGTLRSTEGEDQ 250

236 SFWGDVTHVNGQFWPFKNVEPRKYRFRFLDAAVSRSGLYFADTDADITR 285
      |||||         |||         |||||         |||         |||
251 DLWGDVTHVNGQFWPFLNVQPRKYRFRFLNAAVSRALLYLVRTSSENVNR 300

286 LPFKVIASDGLLEHPADTSLLYISMAERYEVVDFSDYAGKTIELRLNG 335
      || ||||| ||| | ||| || |||||         |||         |||
301 IPFQVIASDAGLLQAPVQTSNLYLAVAERYEIIIDFTINFAGQTLDLRNV. 349

336 GSIGGIGITDIDYDNDKVMRFVADDTTQPDTSWPANLRDVPFSPPTIN 385
      | | | | |||||         | | | | |||||
350 AETNDVGEDEYARTILEVMRFVSSGTVE.DNSQVPSTLRDVPFPPHKEG 398

386 .TPRQFRFRGTGTWTINGVAFADVQNRLLANVPVGTIVERWELINAGNGW 434
      | | | | ||| ||| ||| |||||         |||         |||
399 PADKHFKFERSNGHYLINDVGFADVNERVLAKPELGTVEWELNSSGGW 448

435 THPIHHLVDFKVISRTSGNNARTVMPYES.GLKDWWLGRRETVVWEAH 483
      || ||||| ||| | |||||         |||||         |||
449 SHPVHHLVDFKILKRTGGRG..QVMPYESAGLKDWWLGRGETLTIEAH 496

484 YAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGYNATVFVDPMEELWQ 533
      | | | | |||||         |||         |||         |||
497 YQPWIGAYMAHCHNLIHEDNDMAVFNVTAMEEKGYLQEDFEDPMNPKWR 546

534 ARPYELGEFQAQSGQFSVQAVTERIQTMAEYRYPYAAADE..... 572
      | | | | |||         | | | | |||
547 AVPYNRNDFHARAGNFSAESITARVQELAEQEPYNRLDEILEDLGIEE 594

```

Figure 3: protein sequences alignment of Bilirubin oxidase (top sequence) with Stachybotrys oxidase (bottom sequence).

Figure 3

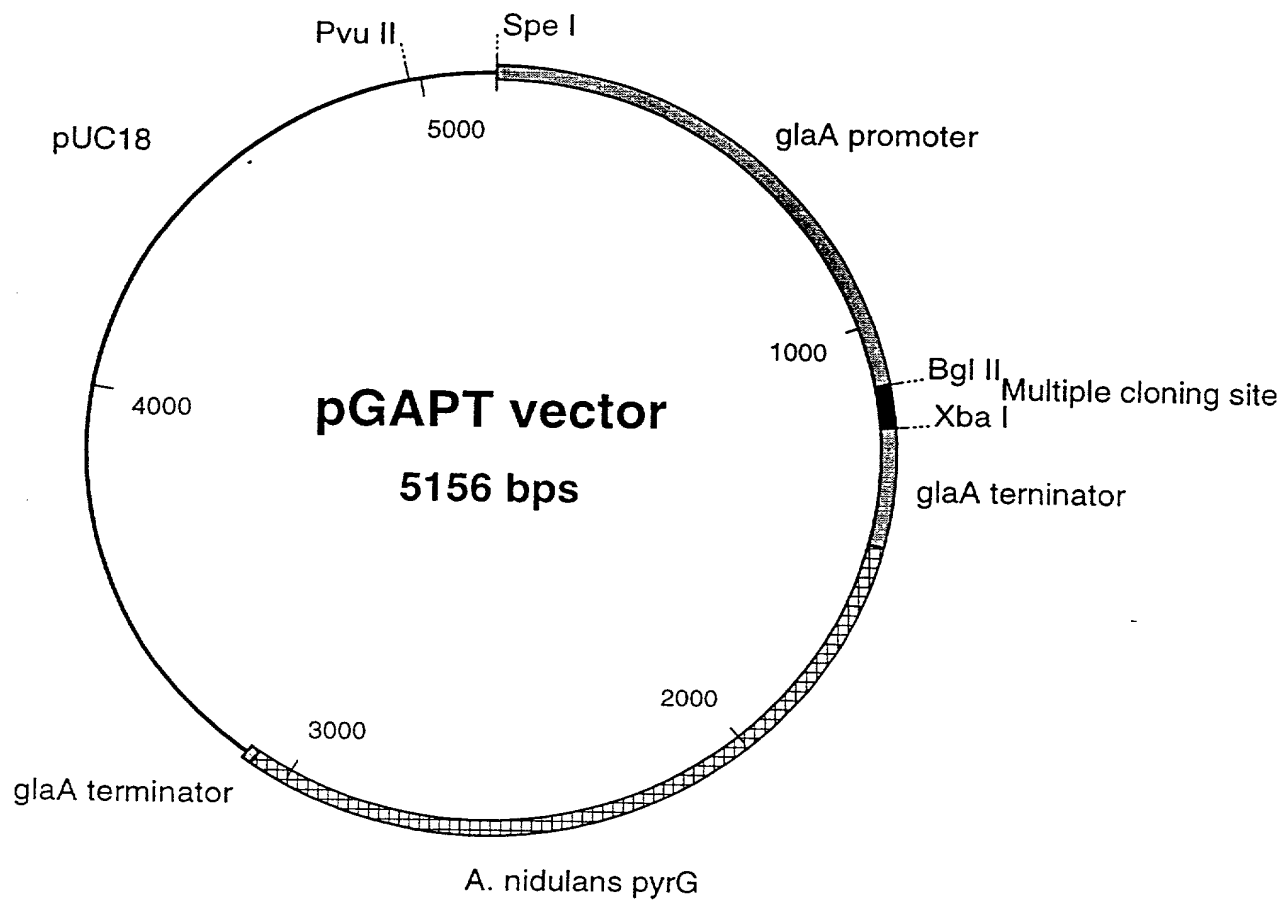


Figure 4

AGATCTAATA	TGCTGTTCAA	GTCATGGCAA	CTGGCAGCAG	CCTCCGGGCT	CCTGTCCTGA	60
GTCTCTGGCA	TCCCGATGGA	CACCGGCAGC	CACCCCATTG	AGGCTGTTGA	TCCCGAAGTG	120
AAGACTGAGG	TCTTCGCTGA	CTCCCTCCTT	GCTGCAGCAG	GCGATGACGA	CTGGGAGTCA	180
CCTCCATACA	ACTTGCTTTA	CAGGTGAGAC	ACCTGTCCCA	CCTGTTTTTC	CTCGATAACT	240
AACTCTTATA	GGAATGCCCT	GCCAATTCCA	CCTGTCAAGC	AGCCCAAGAT	GTATGTCTTT	300
GATTTTCTAC	GAAGCAACTC	GGCCCCGACT	AATGTATTCT	AGGATCATTA	CCAACCTGT	360
CACCGGCAAG	GACATTTGGT	ACTATGAGAT	CGAGATCAAG	CCATTTTCAGC	AAAGGGTGAG	420
TTTGCTCAGA	AACCTTGTGG	TAATTAATCA	TTGTTACTGA	CCCTTTTCAGA	TTTACCCAC	480
CTTGCGCCCT	GCCACTCTCG	TCGGCTACGA	TGGCATGAGC	CCTGGTCCCTA	CTTTCAATGT	540
TCCCAGAGGA	ACAGAGACTG	TAGTTAGGTT	CATCAACAAT	GCCACCGTGG	AGAACTCGGT	600
CCATCTGCAC	GGCTCCCCAT	CGCGTGCCCC	TTTCGATGGT	TGGGCTGAAG	ATGTGACCTT	660
CCCTGGCGAG	TACAAGGATT	ACTACTTTTC	CAACTACCAA	TCCGCCCCGCC	TTCTGTGGTA	720
CCATGACCAC	GCTTTTCATGA	AGGTATGCTA	CGAGCCTTTA	TCTTTCTTGG	CTACCTTTGG	780
CTAACCAACT	TCTTTTCGTA	GACTGCTGAG	AATGCCTACT	TTGGTCAGGC	TGGCGCCTAC	840
ATTATCAACG	ACGAGGCTGA	GGATGCTCTC	GGTCTTCCCTA	GTGGCTATGG	CGAGTTTCGAT	900
ATCCCTCTGA	TCTTGACGGC	CAAGTACTAT	AACGCCGATG	GTACCTTCGG	TTTCGACCGAG	960
GGTGAGGACC	AGGACCTGTG	GGGAGATGTC	ATCCATGTCA	ACGGACAGCC	ATGGCCTTTC	1020
CTTAACGTCC	AGCCCCGCAA	GTACCGTTTC	CGATTCCCTCA	ACGCTGCCGT	GTCTCGTGCT	1080
TGGCTCCTCT	ACCTCGTCAG	GACCAGCTCT	CCCAACGTCA	GAAATCCTTT	CCAAGTCATT	1140
GCCTCTGATG	CTGGTCTCCT	TCAAGCCCCC	GTCAGACCT	CTAACCTCTA	CCTTGCTGTT	1200
GCCGAGCGTT	ACGAGATCAT	TATTGGTATG	CCCTCCCCCTC	TCACGAATGA	GTCAAGAACT	1260
CTAAGACTAA	CACTTGTAGA	CTTCACCAAC	TTTGCTGGCC	AGACTCTTGA	CCTGCGCAAC	1320
GTGCTGAGA	CCAACGATGT	CGGCGACGAG	GATGAGTACG	CTCGCACTCT	CGAGGTGATG	1380
CGCTTCGTGG	TCAGCTCTGG	CACCTGTTGAG	GACAACAGCC	AGGTCCCCCTC	CACCTCTCCGT	1440
GACGTTCCCT	TCCCTCCTCA	CAAGGAAGGC	CCCGCCGACA	AGCACTTCAA	GTTTGAACGC	1500
AGCAACGGAC	ACTACCTGAT	CAACGATGTT	GGCTTTGCCG	ATGTCAATGA	GCGTGTCCCTG	1560
GCCAAGCCCC	AGCTCGGCAC	CGTTGAGGTC	TGGGAGCTCG	AGAACTCCTC	TGGAGGCTGG	1620
AGCCACCCCC	TCCACATTCA	CCTTGTTTGAC	TTCAAGATCC	TCAAGCGAAC	TGGTGGTCTGT	1680
GGCCAGGTCA	TGCCCTACGA	GTCTGCTGGT	CTTAAGGATG	TCGTCTGGTT	GGGCAGGGGT	1740
GAGACCTGA	CCATCGAGGC	CCACTACCAA	CCCTGGACTG	GAGCTTACAT	GTGGCACTGT	1800
CACAACCTCA	TTACAGAGGA	TAACGACATG	ATGGCTGTAT	TCAACGTAC	CGCCATGGAG	1860
GAGAAGGGAT	ATCTTCAGGA	GGACTTCGAG	GACCCCATGA	ACCCCAAGTG	GCGCGCCGTT	1920
CCTTACAACC	GCAACGACTT	CCATGCTCGC	GCTGGAAACT	TCTCCGCGCA	GTCCATCACT	1980
GCCCCGAGTG	AGGAGCTGGC	CGAGCAGGAG	CCGTACAACC	GCCTCGATGA	GATCCTGGAG	2040
GATCTTGGAA	TCGAGGAGTA	GTCTAGA				2067

Figure 5

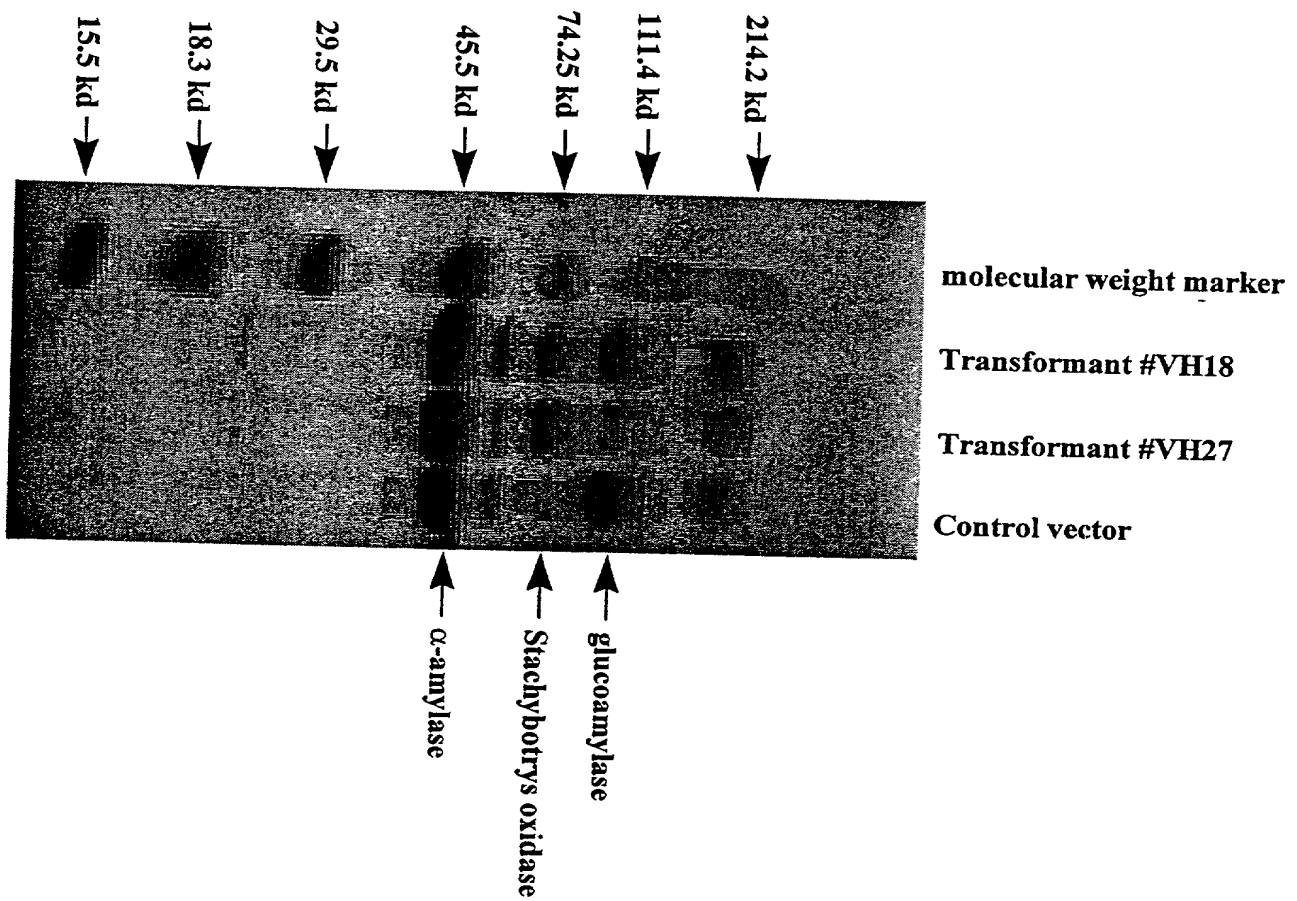


Figure 6